

# Microbial Carbon Use Efficiency Predicted from Genome-scale Metabolic Models

## Background/objective

Characterizing variation in microbial carbon use efficiency (CUE) across taxa and substrate types is key to predicting soil responses to global change.

## Approach

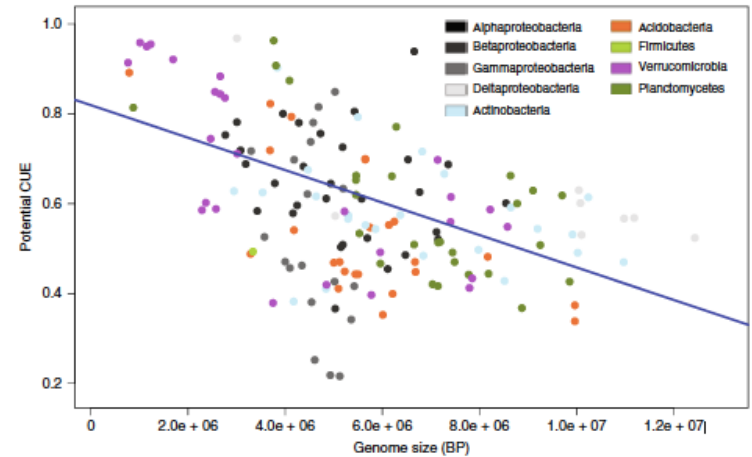
- ❖ Generated theoretical predictions of CUE for more than 200 taxa using genome-scale constraint-based metabolic modeling.
- ❖ Used genome-scale metabolic models to predict microbial physiology based on genes.
- ❖ Developed hypotheses on CUE structure across taxa and substrate types.

## Results

- ❖ A wide range in average potential CUE ( $0.62 \pm 0.17$ ) across taxa with structuring at subphylum levels.
- ❖ Potential CUE declines with increasing genome size, while larger genomes are able to access a wider range of C substrate types.

## Significance

- ❖ These findings provide a framework for predicting CUE from genomic traits and for inferring potential impacts of shifts in bacterial community composition on C cycling.
- ❖ Phylogenetic variation in microbial CUE can dramatically alter patterns in soil C cycling over time.



Potential CUE versus genome size. Potential CUE regressed against genome size (bp). Blue lines show GLS fit. Points are colored by phylum.